

# STIC Biotechnology Systems Branch

## RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 101500,872  
Source: PCT  
Date Processed by STIC: 2-17-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

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Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/500,872

DATE: 02/17/2005

TIME: 12:20:46

Input Set : A:\NOB-8 Seq List (28902.0008).txt  
 Output Set: N:\CRF4\02172005\J500872.raw

4 <110> APPLICANT: OP DEN CAMP, Hubertus Johannes Marie  
 5 HARHANGI, Harry Ramanoedj  
 6 VAN DER DRIFT, Christiaan  
 7 PRONK, Jacobus Thomas  
 9 <120> TITLE OF INVENTION: Fermentation of pentose sugars  
 11 <130> FILE REFERENCE: 28902.0008  
 13 <140> CURRENT APPLICATION NUMBER: 10/500,872  
 14 <141> CURRENT FILING DATE: 2004-07-07  
 16 <150> PRIOR APPLICATION NUMBER: PCT/NL03/00049  
 17 <151> PRIOR FILING DATE: 2003-01-23  
 19 <150> PRIOR APPLICATION NUMBER: BO 44829  
 20 <151> PRIOR FILING DATE: 2001-12-31  
 22 <160> NUMBER OF SEQ ID NOS: 4  
 24 <170> SOFTWARE: PatentIn Ver. 2.1

100% Right  
 Corrected  
 (pg.2-4) ↲

## ERRORED SEQUENCES

26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 437  
 28 <212> TYPE: PRT  
 29 <213> ORGANISM: Piromyces sp.  
 31 <400> SEQUENCE: 1  
 33 Met Ala Lys Glu Tyr Phe Pro Gln Ile Gln Lys Ile Lys Phe Glu Gly  
 34 1 5 10 15  
 36 Lys Asp Ser Lys Asn Pro Leu Ala Phe His Tyr Tyr Asp Ala Glu Lys  
 37 20 25 30  
 39 Glu Val Met Gly Lys Lys Met Lys Asp Trp Leu Arg Phe Ala Met Ala  
 40 35 40 45  
 42 Trp Trp His Thr Leu Cys Ala Glu Gly Ala Asp Gln Phe Gly Gly  
 43 50 55 60  
 45 Thr Lys Ser Phe Pro Trp Asn Glu Gly Thr Asp Ala Ile Glu Ile Ala  
 46 65 70 75 80  
 48 Lys Gln Lys Val Asp Ala Gly Phe Glu Ile Met Gln Lys Leu Gly Ile  
 49 85 90 95  
 51 Pro Tyr Tyr Cys Phe His Asp Val Asp Leu Val Ser Glu Gly Asn Ser  
 52 100 105 110  
 54 Ile Glu Glu Tyr Glu Ser Asn Leu Lys Ala Val Val Ala Tyr Leu Lys  
 55 115 120 125  
 57 Glu Lys Gln Lys Glu Thr Gly Ile Lys Leu Leu Trp Ser Thr Ala Asn  
 58 130 135 140  
 60 Val Phe Gly His Lys Arg Tyr Met Asn Gly Ala Ser Thr Asn Pro Asp  
 61 145 150 155 160

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63 Phe Asp Val Val Ala Arg Ala Ile Val Gln Ile Lys Asn Ala Ile Asp  
64 165 170 175  
E--> 66 Ala Gly Ile Glu Leu Gly Ala Glu Asn Tyr Val Phe Trp Gly Gly Arq  
67 180 185 190  
69 Glu Gly Tyr Met Ser Leu Leu Asn Thr Asp Gln Lys Arg Glu Lys Glu  
70 195 200 205  
72 His Met Ala Thr Met Leu Thr Met Ala Arg Asp Tyr Ala Arg Ser Lys  
73 210 215 220  
75 Gly Phe Lys Gly Thr Phe Leu Ile Glu Pro Lys Pro Met Glu Pro Thr  
76 225 230 235 240  
78 Lys His Gln Tyr Asp Val Asp Thr Glu Thr Ala Ile Gly Phe Leu Lys  
79 245 250 255  
81 Ala His Asn Leu Asp Lys Asp Phe Lys Val Asn Ile Glu Val Asn His  
82 260 265 270  
84 Ala Thr Leu Ala Gly His Thr Phe Glu His Glu Leu Ala Cys Ala Val  
85 275 280 285  
87 Asp Ala Gly Met Leu Gly Ser Ile Asp Ala Asn Arg Gly Asp Tyr Gln  
88 290 295 300  
90 Asn Gly Trp Asp Thr Asp Gln Phe Pro Ile Asp Gln Tyr Glu Leu Val  
91 305 310 315 320  
93 Gln Ala Trp Met Glu Ile Ile Arg Gly Gly Phe Val Thr Gly Gly  
94 325 330 335  
96 Thr Asn Phe Asp Ala Lys Thr Arg Arg Asn Ser Thr Asp Leu Glu Asp  
97 340 345 350  
99 Ile Ile Ile Ala His Val Ser Gly Met Asp Ala Met Ala Arg Ala Leu  
100 355 360 365  
102 Glu Asn Ala Ala Lys Leu Leu Gln Glu Ser Pro Tyr Thr Lys Met Lys  
103 370 375 380  
105 Lys Glu Arg Tyr Ala Ser Phe Asp Ser Gly Ile Gly Lys Asp Phe Glu  
106 385 390 395 400  
108 Asp Gly Lys Leu Thr Leu Glu Gln Val Tyr Glu Tyr Gly Lys Lys Asn  
109 405 410 415  
111 Gly Glu Pro Lys Gln Thr Ser Gly Lys Gln Glu Leu Tyr Glu Ala Ile  
112 420 425 430  
114 Val Ala Met Tyr Gln  
115 435  
182 <210> SEQ ID NO: 3  
183 <211> LENGTH: 494  
184 <212> TYPE: PRT  
185 <213> ORGANISM: Piromyces sp.  
187 <400> SEQUENCE: 3  
189 Met Lys Thr Val Ala Gly Ile Asp Leu Gly Thr Gln Ser Met Lys Val  
190 1 5 10 15  
192 Val Ile Tyr Asp Tyr Glu Lys Lys Glu Ile Ile Glu Ser Ala Ser Cys  
193 20 25 30  
195 Pro Met Glu Leu Ile Ser Glu Ser Asp Gly Thr Arg Glu Gln Thr Thr  
196 35 40 45  
198 Glu Trp Phe Asp Lys Gly Leu Glu Val Cys Phe Gly Lys Leu Ser Ala  
199 50 55 60

INVALID  
AMINO  
ACID

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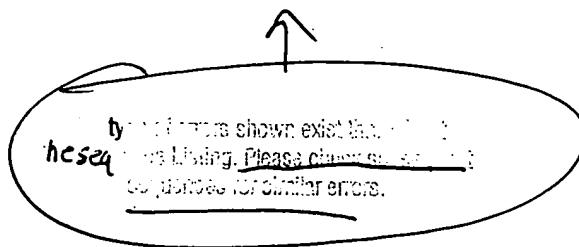
201 Asp Asn Lys Lys Thr Ile Glu Ala Ile Gly Ile Ser Gly Gln Leu His  
 202 65 70 75 80  
 204 Gly Phe Val Pro Leu Asp Ala Asn Gly Lys Ala Leu Tyr Asn Ile Lys  
 205 85 90 95  
 207 Leu Trp Cys Asp Thr Ala Thr Val Glu Glu Cys Lys Ile Ile Thr Asp  
 208 100 105 110  
 210 Ala Ala Gly Gly Asp Lys Ala Val Ile Asp Ala Leu Gly Asn Leu Met  
 211 115 120 125  
 213 Leu Thr Gly Phe Thr Ala Pro Lys Ile Leu Trp Leu Lys Arg Asn Lys  
 214 130 135 140  
 216 Pro Glu Ala Phe Ala Asn Leu Lys Tyr Ile Met Leu Pro His Asp Tyr  
 217 145 *What is this?* 150 155 160  
 219 Leu Asn Trp Lys Leu Thr Gly Asp Tyr Val Met Glu Tyr Gly Asp Ala  
 220 165 170 175  
 E--> 222 Ser Gly Thr A h Leu Phe Asp Ser Lys Asn Arg, Cys Trp Ser Lys Lys  
 E--> 223 180 185 190  
 E--> 225 Ile Cys Asp Ile Ile Asp Pro Lys Leu Leu Asp Leu Leu Pro Lys Leu  
 E--> 226 195 200 205  
 E--> 228 Ile Glu Pro Ser Ala Pro Ala Gly Lys Val Asn Asp Glu Ala Ala Lys  
 E--> 229 210 215 220  
 E--> 231 Ala Tyr Gly Ile Pro Ala Gly Ile Pro Val Ser Ala Gly Gly Asp  
 E--> 232 225 230 235 240  
 E--> 234 Asn Met Met. Gly Ala Val Gly Thr Gly Thr Val Ala Asp Gly Phe Leu  
 E--> 235 245 250 255  
 E--> 237 Thr Met Ser Met Gly Thr Ser Gly Thr Leu Tyr Gly Tyr Ser Asp Lys  
 E--> 238 260 265 270  
 E--> 240 Pro Ile Ser Asp Pro Ala Asn Gly Leu Ser Gly Phe Cys Ser Ser Thr  
 E--> 241 275 280 285  
 E--> 243 Gly Gly Trp Leu Pro Leu Leu Cys Thr Met Asn Cys Thr Val Ala Thr  
 E--> 244 290 295 300  
 E--> 246 Glu Phe Val Arg Asn Leu Phe Gln Met Asp Ile Lys Glu Leu Asn Val  
 E--> 247 305 310 315 320  
 E--> 249 Glu Ala Ala Lys Ser Pro Cys Gly Ser Glu Gly Val Leu Val Ile Pro  
 E--> 250 325 330 335 *ASN*  
 E--> 252 Phe Phe Asn Gly Glu Arg Thr Pro Asn Leu Pro *Asn* Gly Arg Ala Ser  
 E--> 253 340 345 350  
 E--> 255 Ile Thr Gly Leu Thr Ser Ala Asn Thr Ser Arg Ala Asn Ile Ala Arg  
 E--> 256 355 360 365  
 E--> 258 Ala Ser Phe Glu Ser Ala Val Phe Ala Met. Arg Gly Gly Leu Asp Ala  
 E--> 259 370 375 380  
 E--> 261 Phe Arg Lys Leu Gly Phe Gln Pro Lys Glu Ile Arg Leu Ile Gly Gly  
 E--> 262 385 390 395 400  
 E--> 264 Gly Ser Lys-Ser-Asp-Leu-Trp Arg Gln Ile Ala Ala Asp Ile Met Asn  
 E--> 265 405 410 415  
 E--> 267 Leu Pro Ile Arg Val Pro Leu Leu Glu Ala Ala Ala Leu Gly Gly  
 E--> 268 420 425 430  
 E--> 270 Ala Val Gln Ala Leu Trp Cys Leu Lys Asn Gln Ser Gly Lys. Cys Asp  
 E--> 271 435 440 445  
 E--> 273 Ile Val Glu Leu Cys Lys Glu His Ile Lys Ile Asp Glu Ser Lys Asn

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OK  
E 274 450 455 460 Lys  
K 276 Ala Asn Pro Ile Ala Glu Asn Val Ala Val Tyr Asp LYS Ala Tyr Asp  
E 277 465 470 475 480  
K 279 Glu Tyr Cys Lys Val Val Asn Thr Leu Ser Pro Leu Tyr Ala  
E 280 485 490



VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/500,872

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TIME: 12:20:47

Input Set : A:\NOB-8 Seq List (28902.0008).txt  
Output Set: N:\CRF4\02172005\J500872.raw

L:66 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1 ✓  
L:222 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓  
L:222 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:2 ✓  
L:223 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3 ✓  
M:332 Repeated in SeqNo=3  
L:252 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:252 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:3 ✓  
L:280 M:252 E: No. of Seq. differs, <211> LENGTH:Input:494 Found:497 SEQ:3 ✓